

Delaval, Jan

From: Jamroz, Margaret
Sent: Monday, March 25, 2002 8:29 AM
To: Delaval, Jan
Subject: 09/628,126

Jan,

Please do open search of SEQ ID NO: 23 with interference of 09/628,126.

Thanks,

Megan Jamroz

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Margaret.Jamroz@USPTO.gov

Jan Delaval
Reference Librarian
Biotechnology & Chemical Library
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ian.delaval@uspto.gov

Access DB# 63048**SEARCH REQUEST FORM**

Scientific and Technical Information Center

Requester's Full Name: _____ Examiner #: _____ Date: _____
Art Unit: _____ Phone Number 30 _____ Serial Number: _____
Mail Box and Bldg/Room Location: _____ Results Format Preferred (circle): PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need.

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: _____

Inventors (please provide full names): _____

Earliest Priority Filing Date: _____

**For Sequence Searches Only* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.*

Jan Delaval
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Biotechnology & Chemical Library
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STAFF USE ONLYSearcher: JanSearcher Phone #: 6448

Searcher Location: _____

Date Searcher Picked Up: 3/25/02Date Completed: 3/25/02

Searcher Prep & Review Time: _____

Clerical Prep Time: 10Online Time: 10**Type of Search**

NA Sequence (#) _____

AA Sequence (#) ☒

Structure (#) _____

Bibliographic _____

Litigation _____

Fulltext _____

Patent Family _____

Other _____

Vendors and cost where applicable

STN _____

Dialog _____

Questel/Orbit _____

Dr.Link _____

Lexis/Nexis _____

Sequence Systems ☒

WWW/Internet _____

Other (specify) _____

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OM protein - protein search, using sw model

Run on: March 25, 2002, 08:35:55 ; Search time 18.44 Seconds

(without alignments)
888.152 Million cell updates/sec

Title: US-09-628-126-23

Perfect score: 1118

Sequence: 1 MHVPAGSVASHLGTTSRSYF.....DTSTFPLENVLISFLYSNSD 215

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Minimum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR1.*

2: PIR2.*

3: PIR3.*

4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1118	100.0	234	2 A40710	CD30 ligand - huma
2	814.5	72.9	239	2 B40710	CD30 ligand - mous
3	112	10.0	279	2 A53062	Fas ligand - mouse
4	96.5	8.6	234	1 J01344	tumor necrosis fac
5	94	8.4	235	2 I34900	tumor necrosis fac
6	93.5	8.4	547	2 T30704	rifampicin resista
7	90.5	8.1	281	2 I38707	Fas ligand - human
8	90	8.1	233	1 S22052	tumor necrosis fac
9	89	8.0	809	2 T38051	hypothetical prote
10	87.5	7.8	813	2 T12506	hypothetical prote
11	86	7.7	278	2 A49286	fas ligand - rat
12	85.5	7.6	309	2 I53384	4-1BB ligand - mou
13	85	7.6	235	1 QWMSN	tumor necrosis fac
14	84.5	7.6	232	1 S12606	tumor necrosis fac
15	83.5	7.5	234	1 JH0529	tumor necrosis fac
16	83	7.4	636	2 S70877	hypothetical prote
17	83	7.4	1385	2 T18213	paraspinal crystal
18	82	7.3	513	2 B96524	hypothetical prote
19	82	7.3	1339	2 G84764	hypothetical prote
20	81.5	7.3	461	2 JN0129	ID-myo-inositol-tr
21	81	7.2	233	1 QWHUN	tumor necrosis fac
22	81	7.2	547	2 H65107	hypothetical 61.6
23	81	7.2	1289	2 T18212	paraspinal crystal
24	80.5	7.2	430	2 T28318	ORF MSV157 hypothe
25	80.5	7.2	434	1 S61999	hypothetical prote
26	80.5	7.2	499	2 A55346	phosphoprotein pho
27	80	7.2	235	2 JH0029	tumor necrosis fac
28	79.5	7.1	233	1 S24642	tumor necrosis fac
29	79	7.1	800	2 S53079	PET111 protein - y

30 78.5 7.0 426 2 S64748
31 78.5 7.0 1130 2 T29089
32 78.5 7.0 1830 2 E82909
33 77.5 6.9 492 2 S42735
34 77.5 6.9 610 2 S71758
35 77.5 6.9 623 2 B96681
36 77 6.9 329 2 T28412
37 77 6.9 456 2 B96688
38 76.5 6.8 478 2 T27714
39 76.5 6.8 619 2 S54636
40 76.5 6.8 3512 2 T17121
41 76 6.8 467 2 D86485
42 76 6.8 479 2 E42508
43 76 6.8 607 2 E70165
44 76 6.8 829 2 S72366
45 75.5 6.8 284 2 F81431

ALIGNMENTS

RESULT 1

A40710

CD30 ligand - human

C.Species: Homo sapiens (man)

C.Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 21-Jul-2000

C.Accession: A40710

R:Smith, C.A.; Gruss, H.J.; Davis, T.; Anderson, D.; Farrah, T.; Baker, E.; Sutherland,

Alderson, M.; Falk, B.; Gimpel, S.; Gillis, S.; Din, W.S.; Girdwin, R.G.; Armitage,

Cell 73, 1349-1360, 1993

A>Title: CD30 antigen, a marker for Hodgkin's lymphoma, is a receptor whose ligand de

A:Reference number: A40710; MUID:93313964

A:Accession: A40710

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-234 <SMI>

A:Cross-references: GB:109753; NID:g349277; PIDN:AAA74594.1; P: f349278

C:Keywords: cytokine receptor; membrane protein; surface antigen

Query Match 100.0%; Score 1118; DB 2; Length 234;
Best Local Similarity 100.0%; Pred. No. 2.4e-98;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHVPAGSVASHLGTTSRSYFYLTTATLALCLVFTVATIMVLVQRTDSIPK...DNVPLKG 60

DB 20 MHVPAGSVASHLGTTSRSYFYLTTATLALCLVFTVATIMVLVQRTDSIPK...NVPLKG 79

QY 61 GNCSEDLCLIKRAPKKSWAYLQVAKHLNKTLSWKNKDGILHGVRYQDC...TQFPGLY 120

DB 80 GNCSEDLCLIKRAPKKSWAYLQVAKHLNKTLSWKNKDGILHGVRYQDC...TQFPGLY 139

QY 121 FITCOLFVOCNPNNSVDLKLLELHINKHKKOALVTYCESGMOTKHVYQNLSC...EDYLO 180

DB 140 FITCOLFVOCNPNNSVDLKLLELHINKHKKOALVTYCESGMOTKHVYQNL...EDYLO 199

QY 181 VNTTISVNDVTFQYIDTSTFPLENVLISFLYSNSD 215

DB 200 VNTTISVNDVTFQYIDTSTFPLENVLISFLYSNSD 234

RESULT 2

B40710

CD30 ligand - mouse

C.Species: Mus musculus (house mouse)

C.Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 05-Nov-1999

C.Accession: B40710

R:Smith, C.A.; Gruss, H.J.; Davis, T.; Anderson, D.; Farrah, T.; Baker, E.; Sutherland,

Alderson, M.; Falk, B.; Gimpel, S.; Gillis, S.; Din, W.S.; Girdwin, R.G.; Armitage,

Cell 73, 1349-1360, 1993

A>Title: CD30 antigen, a marker for Hodgkin's lymphoma, is a receptor whose ligand de

A:Reference number: A40710; MUID:93313964

A:Accession: B40710

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QY      18 SYFYLTATLALCLVTFVTATIMVLVVQRTDSIENSQDNVPLKGCNCSEDI.LC.ILKBPFK 77
Db      37 SFLVAGATTFLCL-----NFGVIGPQREKEFFN---NLPIIGSMAQTILQLRSESSNSSD 89

QY      78 KSWAYLQVAHKLAKTKLSWNKDG-----ILHGVRVQDGNLVIOPGGLYFIITGLOFIVVO-C 132
Db      90 KPVAHV-VANHQVDEOLEWLSRGANALLANGMDLKNOLVIPADGLYLVLV1122LFLKGQC 148

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Immunogenetics 35, 351-353, 1992
A:Title: Sequence of the tumor necrosis factor/cachectin (TNF) gene from Peromyscus
A:Reference number: I54490; MUID:92218012
A:Accession: I54490
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-235 <RES>
A:Cross-references: GB:M59233; NID:g202506; PIDN:AAA40596.1; PID:g202507
C:Genetics:
A:Gene: PltNF
A:Introns: 62/3; 81/1; 97/1
C:Superfamily: tumor necrosis factor
C:Keywords: glycoprotein; lipoprotein; myristylation
F:19/20/Binding site: myristate (Lys) (covalent) #status predicted
F:84/Binding site: carbohydrate (Ser) (covalent) #status predicted

Query Match      8.43;   Score 94;   DB 2;   Length 275.
Best Local Similarity 24.08;   Pred. No. 0.18;
Matches 48;   Conservative 31;   Mismatches 85;   Indels 36;   Gaps 8;

QY 18 SYFVLTTATLALCLVFTVATIMLVVQVQTDSPNSPDNVPLKGCNCSDDLGLCKRAPFK 77
      | : : | | | | : | : | : | : | : | : | : | : | : | : | : | : |
Db 37 SFLLVAGATTFLCLL-----NFGVICPQREERFPN---NLPIGCSMAQTLLRSSQSSSD 89

QY 78 KSNAYLOVAKHLNKTLSWNKDG-----ILHGVRVYQDGNLVIOFPGLYFIICGLIOFLVO-C 132
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 90 KPAVHV-VANHQVDEQLEWLSRGANALLANGMDLKDNLVIPADGLYLVVYGLFEGQGC 148

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FT CARBOHYD 189 189 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 201 201 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 234 AA; 26017 MW; C653615682305BIB CRC64;

Query Match
Best Local Similarity 100.0%; Score 1118; DB 1; Length 234;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHVPAGSVASHLGTTSRSYFLTTATLALCLVFTVATIMVLVQRTSDIPNSPNVPLKG 60
    |||||F|||||
DB 20 MHVPAGSVASHLGTTSRSYFLTTATLALCLVFTVATIMVLVQRTSDIPNSPNVPLKG 79
    |||||F|||||

QY 61 GNCSEDLCLIKRAPFKSWAYLOVAKHLNKTLSWKNKDGILHGVRYODGNLVIQFPGLY 120
    |||||F|||||
DB 80 GNCSEDLCLIKRAPFKSWAYLOVAKHLNKTLSWKNKDGILHGVRYODGNLVIQFPGLY 139
    |||||F|||||

QY 121 FIICOLFVQCPNNSVDLKLLELINKHKKQALVTVCSGMOTKHVYQNLQSFLDYLO 180
    |||||F|||||
DB 140 FIICOLFVQCPNNSVDLKLLELINKHKKQALVTVCSGMOTKHVYQNLQSFLDYLO 199
    |||||F|||||

QY 181 VNTTISVNDTFQYIDTSTFPLENLSIFLYSNSD 215
    |||||F|||||
DB 200 VNTTISVNDTFQYIDTSTFPLENLSIFLYSNSD 234
    |||||F|||||

RESULT 2
TNF8_MOUSE
ID TNF8_MOUSE STANDARD; PRT; 239 AA.
AC P32972;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE CD30 LIGAND (CD30-L).
GN TNFSF8 OR CD30LG OR CD30L.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=93313964; PubMed=8391931;
RA Smith C.A., Gruesh H.-J., Davis T., Anderson D., Farrah T.,
RA Baker E., Sutherland G.R., Brannan C.I., Copeland N.G., Jenkins N.A.,
RA Grabstein K.H., Gliniak B., McAlister I.B., Fanslow W., Alderson M.,
RA Falk B., Gimpel S., Gillis S., Din W.S., Goodwin R.G., Armitage R.J.;
RT "CD30 antigen, a marker for Hodgkin's lymphoma, is a receptor whose
RT ligand defines an emerging family of cytokines with homology to
RT TNF.";
RL Cell 73:1349-1360(1993).
CC -|- FUNCTION: BINDS TO THE CD30 RECEPTOR. INDUCES PROLIFERATION OF
CC T CELLS.
CC -|- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN.
CC -|- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC the European Bioinformatics Institute. There are no restrictions on its
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CC -----
CC EMBL; L09754; AAA74595.1;
CC PIR; B40710; B40710.
CC MGD; MGI:88328; Tnfsf8.
CC InterPro; IPR003638; TNF_8.
CC InterPro; IPR000478; TNF_family.
CC Pfam; PF00229; TNF; 1.
CC ProDom; PD023087; TNF_8; 1.
CC SMART; PS00207; TNF; 1.
CC PROSITE; PS00251; TNF_1; 1.
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DR PROSITE; PS00049; TNF_2; 1.
KW Cytokine; Transmembrane; Glycoprotein; Signal-anchor.
FT DOMAIN 1 43 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 44 67 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
FT DOMAIN 68 239 EXTRACELLULAR (POTENTIAL).
FT CARBOHYD 75 75 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 86 86 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 114 114 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 158 158 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 194 194 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 206 206 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 239 AA; 26519 MW; 29003157DD425159 CRC64;

Query Match
Best Local Similarity 72.9%; Score 814.5; DB 1; Length 239;
Matches 156; Conservative 26; Mismatches 32; Indels 7; Gaps 2;

QY 1 MHVPAGSVAS-----HLGTTTSRSYFLTTATLALCLVFTVATIMVLVQRTSDIPNSPD 54
    |||||F|||||
DB 20 MQVQPGSVASVWRSTRPWRSTRPWRSTRPWRSTRPWRSTRPWRSTRPWRSTRPWRSTRP 78
    |||||F|||||

QY 55 NVPLKGGNCSEDLCLIKRAPFKSWAYLOVAKHLNKTLSWKNKDGILHGVRYODGNLVI 114
    |||||F|||||
DB 79 KAPLGGNCSEDLCLIKRAPFKSWAYLOVAKHLNKTLSWKNKDGILHGVRYODGNLVI 138
    |||||F|||||

QY 115 QPGLYFIICOLFVQCPNNSVDLKLLELINKHKKQALVTVCSGMOTKHVYQNLQSOF 174
    |||||F|||||
DB 139 QPGLYFIICOLFVQCPNNSVDLKLLELINKHKKQALVTVCSGMOTKHVYQNLQSOF 198
    |||||F|||||

QY 175 LLDYLVQVNTTISVNDTFQYIDTSTFPLENLSIFLYSNSD 215
    |||||F|||||
DB 199 LLHYLVQVNTTISVNDTFQYIDTSTFPLENLSIFLYSNSD 239
    |||||F|||||

RESULT 3
FASL_MOUSE
ID FASL_MOUSE STANDARD; PRT; 279 AA.
AC P41047; O61217; Q9R1F2;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE FAS ANTIGEN LIGAND.
GN TNFSF6 OR APTLGI OR FASL OR GLD.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM FASL).
RX MEDLINE=94185175; PubMed=7511063;
RA Takahashi T., Tanaka M., Brannan C.I., Jenkins N.A., Copeland N.G.,
RA Suda T., Nagata S.;
RT "Generalized lymphoproliferative disease in mice, caused by a point
RT mutation in the Fas ligand.";
RL Cell 76:969-976(1994).
CC [2]
CC SEQUENCE FROM N.A. (ISOFORM FASL), AND 3D-STRUCTURE MODELLING.
CC STRAIN=C57BL/6;
CC MEDLINE=95388076; PubMed=7544870;
CC Peitsch M.J., Tschopp J.J.;
RT "Comparative molecular modelling of the Fas-ligand and other members
RT of the TNF family.";
RL Mol. Immunol. 32:761-772(1995).
CC [3]
CC SEQUENCE FROM N.A. (ISOFORM FASL).
RX MEDLINE=95196085; PubMed=7889405;
RA Lynch D.H., Watson M.L., Alderson M.R., Baum P.R., Miller R.E.,
RA Tough T., Gibson M., Davis-Smith T., Smith C.A., Hunter K.;
RT "The mouse Fas-ligand gene is mutated in gld mice and is part of a
RT TNF family gene cluster.";
RL Immunity 1:131-136(1994).
CC [4]
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OM protein - protein search, using sw model

Run on: March 25, 2002, 08:37:40 ; Search time 13.96 Seconds
(without alignments)
564.680 Million cell updates/sec

Title: US-09-628-126-23

Perfect score: 1118

Sequence: 1 MHVPAGSVASHLGTTSRSYF.....DTSTFPLENLVLSIFLYNSD 215

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1118	100.0	234	1 TNF8_HUMAN	P32971 homo sapien
2	814.5	72.9	279	1 TNF8_MOUSE	P32972 mus musculus
3	112	10.0	279	1 FASL_MOUSE	P41047 mus musculus
4	96.5	8.6	234	1 TNFA_HORSE	P29553 equus caball
5	94	8.4	233	1 TNFA_MACMU	P48094 macaca mulia
6	94	8.4	235	1 TNFA_PERLE	P36939 peromyscus
7	92	8.2	233	1 TNFA_MACPA	P79337 macaca fasc
8	90.5	8.1	281	1 FASL_HUMAN	P48023 homo sapien
9	90	8.1	233	1 TNFA_PAPHU	O77510 papio hamad
10	90	8.1	233	1 TNFA_PAPSP	P33620 papio sp. (
11	89	8.0	809	1 YATA_SCHPO	Q10155 schizosacch
12	86	7.7	278	1 FASL_RAT	P36940 rattus norv
13	85.5	7.6	309	1 41BL_MOUSE	P41274 mus musculus
14	85	7.6	233	1 TNFA_CANFA	P51742 canis famil
15	85	7.6	235	1 TNFA_MOUSE	P06804 mus musculus
16	85	7.6	1220	1 CSAC_BACTU	P56955 bacillus th
17	84.5	7.6	232	1 TNFA_PIG	P23563 sus scrofa
18	83.5	7.5	234	1 TNFA_SHEEP	P23383 ovis aries
19	83	7.4	1385	1 CSAA_BACUD	Q45760 bacillus th
20	81.5	7.3	461	1 IP3K_HUMAN	P23677 homo sapien
21	81	7.2	233	1 TNFA_HUMAN	P01375 homo sapien
22	81	7.2	233	1 TNFA_MARMO	O35734 marmota mon
23	81	7.2	541	1 YHBX_ECOLI	P42640 escherichia
24	81	7.2	1289	1 CSAB_BACUD	Q45753 bacillus th
25	80.5	7.2	429	1 PPP5_RAT	P53042 rattus norv
26	80	7.2	229	1 TNFA_CEREL	P51743 cervus elap
27	80	7.2	235	1 TNFA_RAT	P16599 rattus norv
28	79.5	7.1	233	1 TNFA_BOVIN	Q06599 bos taurus
29	79	7.1	800	1 P711_YEAST	P08468 saccharomyc
30	78.5	7.0	234	1 TNFA_CAVPO	P51435 cavia porce
31	78.5	7.0	426	1 MMML_YEAST	P41800 saccharomyc
32	77.5	6.9	670	1 DD18_HUMAN	Q9nvp1 homo sapien
33	76	6.8	479	1 PAP1_VACCC	P21079 vaccinia vi

ALIGNMENTS

RESULT 1	1	829	6.8	76	34	TOP1_XENLA
TNF8_HUMAN						
ID: TNF8_HUMAN	STANDARD;	PRT;	234 AA.			
AC P32971;						
DT 01-OCT-1993 (Rel. 27, Created)						
DT 01-OCT-1993 (Rel. 27, Last sequence update)						
DT 20-AUG-2001 (Rel. 40, Last annotation update)						
DE CD30 LIGAND (CD30-L) (CD153 ANTIGEN).						
GN TNFSF8 OR CD30LG OR CD30L.						
OS Homo sapiens (Human).						
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;						
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.						
OX NCBI_TaxID=9606;						
ON [1]						
RP SEQUENCE FROM N.A.						
RX MEDLINE-93313964; PubMed-8391931;						
RA Smith C.A., Gruess H.-J., Davis T., Anderson D., Farrah T.,						
RA Baker E., Sutherland G.R., Brannan C.I., Copeland N.G., Jenkins N.A.,						
RA Grabstein K.H., Gliniak B., McAllister I.B., Fanslow W., Anderson M.,						
RA Falk B., Gimpel S., Gillis S., Din W.S., Goodwin R.G., Armitage R.J.,						
RT CD30 antigen, a marker for Hodgkin's lymphoma, is a receptor whose						
RT ligand defines an emerging family of cytokines with homology to						
TNF.						
RL Cell 73:1349-1360(1993).						
CC -I- FUNCTION: BINDS TO THE CD30 RECEPTOR. INDUCES PROLIFERATION OF						
CC T CELLS.						
CC -I- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN.						
CC -I- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.						
CC -I- DATABASE: NAME=PROW; NOTE=CD guide CD153 entry;						
CC WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd153.htm"						
CC -----						
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CC -----						
CC EMBL; L09753; AAA74594.1; --						
CC DR PIR; A40710; A40710.						
CC DR MIM; 603875; --						
CC InterPro: IPR003639; TNF_8.						
CC DR InterPro: IPR000478; TNF_family.						
CC DR Pfam; PF00229; TNF; 1.						
CC DR ProDom; PD023087; TNF_8; 1.						
CC DR SMART; SM00207; TNF; 1.						
CC DR PROSITE; PS00251; TNF_1; 1.						
CC DR PROSITE; PS00049; TNF_2; 1.						
CC Cytokine; Transmembrane; Glycoprotein; Signal-anchor.						
CC CYTOPLASMIC (POTENTIAL).						
CC DOMAIN 1 37						
CC FT TRANSMEM 38 62						
CC FT DOMAIN 63 234						
CC FT CARBOHYD 81 81						
CC FT CARBOHYD 109 109						
CC FT CARBOHYD 153 153						

P4111 xenopus lae
C01814 sarcophyton
P43010 arabidopsis
P81474 buchnera ap
P53030 homo sapien
P53030 buchnera ap
P53030 escherichia
P53030 saccharomyc
P53030 marchantia
P53030 saccharomyc
C5115 borrelia bu
P37297 saccharomyc

Silt No.	Score	Query, %		Length	DB	ID	Description
		Match					
1	1094	97.9	234	4	O43404	O43404	homo sapien
2	100	8.9	169	11	Q9WV90	Q9WV90	marmota mon
3	96.5	8.6	215	6	Q9BE8	Q9BE8	erinaceus e
4	95.5	8.5	280	6	Q9BDN1	Q9BDN1	cercocebus
5	94.5	8.5	234	6	Q9TJ3	Q9TJ3	equus cabal
6	93.5	8.4	547	12	Q98269	Q98269	molluscum c
7	93	8.3	217	11	Q9ERG6	Q9ERG6	peromyscus
8	92	8.2	280	6	Q9MYL6	Q9MYL6	macaca neme
9	92	8.2	280	6	Q9BDM5	Q9BDM5	macaca mulla
10	89.5	8.0	896	10	Q9M9B0	Q9M9B0	arabidopsia
11	88.5	7.9	217	6	Q9BEG1	Q9BEG1	bradyptu tr
12	88	7.9	1109	5	Q9GYH7	Q9GYH7	caenorhabdi
13	87.5	7.8	216	6	Q9BEC4	Q9BEC4	talpa europ
14	87.5	7.8	813	4	Q9Y4N0	Q9Y4N0	homo sapien
15	87.5	7.8	1003	4	Q9P207	Q9P207	homo sapien
16	85.5	7.6	462	2	Q9CM44	Q9CM44	pasteurella
17	85	7.6	282	6	Q9BEA8	Q9BEA8	scrofa
18	85	7.6	761	3	Q9UVJ1	Q9UVJ1	candida alb
19	84.5	7.6	232	4	Q9UIV3	Q9UIV3	homo sapien

Db 80 GNCSEDLICILKRAPFKSWAYLQVAKHLNKTLSNWKDGIILHGVRQDGNLVIOFPGLY 139
QY 121 FIICLOFLVQCPNNSVDLKLLELLINKHKKKALVTVCSGMOVKHYVQNLQSLDLYLQ 180
Db 140 FIICLOFLVQCPNNSVDLKLLELLINKHKKKALVTVCSGMOVKHYVQNLQSLDLYLQ 199
QY 181 VNTTISVNVDTFOYIDTSTFPLENVLISFLYSNSD 215
Db 200 VNTTISVNVDTFOYIDTSTFPLENVLISFLYSNSD 234
RESULT 2
Q9WV90 PRELIMINARY; PRT; 169 AA.
AC Q9WV90;
DT 01-NOV-1999 (Tremblrel. 12, Created)
RT 01-JUN-2001 (Tremblrel. 12, Last sequence update)
DE FAS LIGAND (FRAGMENT).
OS Marmota monax (Woodchuck).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sclurinae;
OC Marmota.
OX NCBI_TaxID=9995;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=HEALTHY LIVER;
RA Hodgson P.D., Grant M.D., Michalak T.I.;
RT "Perforin and Fas/Fas ligand-mediated cytotoxicity in acute and
chronic woodchuck viral hepatitis";
RL Clin. Exp. Immunol. 0:0-0(1999).
DR EMBL; AF152368; AAD38387.1; -;
DR InterPro; IPR000478; TNF_family.
DR InterPro; IPR003263; TNF_5.
DR Pfam; PF00229; TNF; 1.
DR ProDom; PD008600; TNF_5; 1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS00049; TNF_2; 1.
DR SMART; SM00207; TNF; 1.
FT NON_TER 169 169
FT SEQUENCE 169 AA; 19274 MW; FDE395B014717B6B CRC64;

Query Match 8.9%; Score 100; DB 11; Length 169;
Best Local Similarity 24.6%; Pred. No. 0.025;
Matches 32; Conservative 23; Mismatches 45; Indels 30; Gaps 5;
QY 71 LKRAPFKSWAYLQVAKHLNKTLSNWKD---GILHGVRQDGNLVIOFPGLYFIICLOLQ 127
Db 40 LRRA-----AHLTGKPNRSRSPLEWEDTYGISLSIGVKYQKGLVINDTGLYFYVSKYIY 93
QY 128 FLVQ-CPNNSVDLKLLELLINKH-----IKKQALVTVCSGM-----QTKH 166
Db 94 FRGSCNNQPLSHKYYVKNASKYPQDLVLMCKMKNYCTTGOMWARSSYLGAFFNFTSNDH 153
QY 167 VYQNLQFL 176
Db 154 LYVNVSELSL 163

RESULT 3
ID Q9BEE8 PRELIMINARY; PRT; 215 AA.
AC Q9BEE8;
DT 01-JUN-2001 (Tremblrel. 17, Created)
RT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DE TUMOR NECROSIS FACTOR PRECURSOR (FRAGMENT).
GN TNFA.
OS Erinaceus europaeus (Western European hedgehog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Insectivora; Erinaceidae; Erinaceinae; Erinaceus.
OX NCBI_TaxID=9365;
RN [1]
RP SEQUENCE FROM N.A.
RA van Dijk M.A.M., de Jong W.W.;
RT "Indels indicate that rodents are monophyletic and lagomorphs are
their sister group";
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases
DR EMBL; AJ286830; CAC28522.1; -;
FT NON_TER 1 1
FT NON_TER 215 215
FT SEQUENCE 215 AA; 23696 MW; 3E337E7E65F074EA CRC64;

Query Match 8.6%; Score 96.5; DB 6; Length 133;
Best Local Similarity 23.3%; Pred. No. 0.075;
Matches 47; Conservative 36; Mismatches 76; Indels 43; Gaps 10;
QY 18 SYFLTATATLALCLIVFTVATIMLVQRTDSIPNSPDNVPKGGNCSEDLILK--RAP 75
Db 28 SFLVAGATTFLCLLH---FGVIGPQDE---FPDNIQLNNA-----LAVPLRSSRTQ 74
QY 76 FKSWAYLQVAKHLNKTLSNWKD---ILHGVRQDGNLVIOFPGLYFIICLOLQ 131
Db 75 SDRPVAHV-VASIKSEGLLWSEVANALLANGKLTQNLVPLDGLYL---QVLFKQ 133
QY 132 -CPNNSVDLKLLELLINKHKK-----QALVTVCS-----GMQTHVYQNLQSLQ 174
Db 134 GCPSTHV-----FLTHNKRKYAVSYQKDVNLLSAIKSPCQSETPGEAEAFHWYEPYILG 187
QY 175 LLDYLQVNTTISVNVDTFOYID 196
Db 188 GVQLEKGDRLSAEINLPDYID 209

RESULT 4
Q9BDN1 PRELIMINARY; PRT; 280 AA.
AC Q9BDN1;
DT 01-JUN-2001 (Tremblrel. 17, Created)
RT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DE CD95L PROTEIN.
GN CD95L.
OS Cercopithecus torquatus atys (Red-crowned mangabey) (Sooty mangabey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Cercopithecidae;
OX NCBI_TaxID=9531;
RN [1]
RP SEQUENCE FROM N.A.
RA Villinger F., Bostik P., Mayne A.E., King C.L., Genain C.P.,
Weiss W.R., Ansari A.A.;
RT "Cloning, sequencing and homology analysis of nonhuman Fc gamma 1
Fas/Fas-Ligand and co-stimulatory molecules";
RL Immunogenetics 0:0-0(2001).
DR EMBL; AF344847; AAK37606.1; -;
FT SEQUENCE 280 AA; 31407 MW; 729EA60067B7D398 CRC64;

Query Match 8.5%; Score 95.5; DB 6; Length 280;
Best Local Similarity 27.1%; Pred. No. 0.13;
Matches 35; Conservative 21; Mismatches 46; Indels 27; Gaps 6;
QY 75 PFKKSW---AYLQVAKHLNKTLSNWKD-GI---LHGVRQDGNLVIOFPGLYFIICLOLQ 128
Db 137 PEKQKQKVAHLTKPNRSRSPLEWEDTYGIVLLSGVKYKGLVINDTGLYFYVSKYIY 196
QY 129 LVO-CPNNSVDLKLLELLINKH-----IKKQALVTVCSGM-----QTKHV 167
Db 197 RGQSCNNQPLSHKYYVKNASKYPQDLVLMCKMKNYCTTGOMWARSSYLGAFFNLTSTDHL 256
QY 168 YQNLQSL 176

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 25, 2002, 08:35:55 ; Search time 19.25 Seconds
(without alignments)
251.335 Million cell updates/sec

Title: US-09-628-126-23
Perfect score: 1118
Sequence: 1 MHPAGSVASHLGTTSRSYF.....DTSTFPLENVLSIFLYNSD 215

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0

Minimum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*

1: /cgn2_6/ptodata/2/1aa/5A_COMB.pep.*

2: /cgn2_6/ptodata/2/1aa/5B_COMB.pep.*

3: /cgn2_6/ptodata/2/1aa/6A_COMB.pep.*

4: /cgn2_6/ptodata/2/1aa/6B_COMB.pep.*

5: /cgn2_6/ptodata/2/1aa/PCTUS_COMB.pep.*

6: /cgn2_6/ptodata/2/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1118	100.0	215	1 US-08-225-989-23	Sequence 23, Appl
2	1118	100.0	215	1 US-08-570-923-23	Sequence 23, Appl
3	1118	100.0	215	1 US-08-580-014-23	Sequence 23, Appl
4	1118	100.0	215	4 US-09-079-785-23	Sequence 23, Appl
5	1118	100.0	234	1 US-08-225-989-8	Sequence 8, Appl1
6	1118	100.0	234	1 US-08-570-923-8	Sequence 8, Appl1
7	1118	100.0	234	1 US-08-580-014-8	Sequence 8, Appl1
8	1118	100.0	234	4 US-09-079-785-8	Sequence 8, Appl1
9	814.5	72.9	220	1 US-08-225-989-19	Sequence 19, Appl
10	814.5	72.9	220	1 US-08-570-923-19	Sequence 19, Appl
11	814.5	72.9	220	1 US-08-580-014-19	Sequence 19, Appl
12	814.5	72.9	220	4 US-09-079-785-19	Sequence 19, Appl
13	814.5	72.9	239	1 US-08-225-989-6	Sequence 6, Appl1
14	814.5	72.9	239	1 US-08-570-923-6	Sequence 6, Appl1
15	814.5	72.9	239	1 US-08-580-014-6	Sequence 6, Appl1
16	814.5	72.9	239	4 US-09-079-785-6	Sequence 6, Appl1
17	775	69.3	148	3 US-08-584-031-12	Sequence 12, Appl
18	592	53.0	125	1 US-08-225-989-20	Sequence 20, Appl
19	592	53.0	125	1 US-08-570-923-20	Sequence 20, Appl
20	592	53.0	125	1 US-08-580-014-20	Sequence 20, Appl
21	592	53.0	125	4 US-09-079-785-20	Sequence 20, Appl
22	447.5	40.0	130	1 US-08-225-989-21	Sequence 21, Appl
23	447.5	40.0	130	1 US-08-570-923-21	Sequence 21, Appl
24	447.5	40.0	130	1 US-08-580-014-21	Sequence 21, Appl
25	447.5	40.0	130	4 US-09-079-785-21	Sequence 21, Appl
26	274	24.5	52	4 US-09-369-494-17	Sequence 17, Appl
27	274	24.5	52	4 US-09-358-569D-15	Sequence 15, Appl

28 102 9.1 279 5 PCT-US95-00362-5
29 92 8.2 378 3 US-08-630-172-21
30 92 8.2 378 4 US-09-375-419-21
31 91.5 8.2 376 3 US-08-751-512-8
32 90.5 8.1 145 3 US-08-630-172-5
33 90.5 8.1 145 4 US-09-375-419-5
34 90.5 8.1 179 3 US-08-649-100-9
35 90.5 8.1 281 2 US-08-810-453-2
36 90.5 8.1 281 3 US-08-815-190A-2
37 90.5 8.1 281 4 US-09-290-640-25
38 90.5 8.1 281 4 US-09-479-524-3
39 90.5 8.1 281 5 PCT-US95-00362-2
40 90.5 8.1 287 3 US-08-815-190A-16
41 90 8.1 141 4 US-09-286-529-22
42 90 8.1 149 3 US-08-584-031-17
43 86 7.7 158 1 US-07-994-469A-99
44 85.5 7.6 309 1 US-08-236-918A-2
45 85 7.6 161 1 US-07-994-469A-61

ALIGNMENTS

RESULT 1
US-08-225-989-23
; Sequence 23, Application US/08225989
; Patent No. 5489881
; GENERAL INFORMATION:
; APPLICANT: Goodman, Raymond G.
; APPLICANT: Smith, Craig A.
; APPLICANT: Armistage, Richard J.
; APPLICANT: Gruss, Hans-Jurgen
; TITLE OF INVENTION: No. 5480981el Cytokine That Binds
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kathryn A. Seese, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98101

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple 7.1
; SOFTWARE: Microsoft Word, Version 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/225,989
; FILING DATE: 12 APRIL 1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/966,775
; FILING DATE: 27-OCT-1992
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 907,224
; FILING DATE: 01-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 899,660
; FILING DATE: 15-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 892,459
; FILING DATE: 02-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 889,717
; FILING DATE: 26-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Seese, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2804-E
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644

TELEX: 756822
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 215 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-225-989-23

Query Match 100.0%; Score 1118; DB 1; Length 215;
Best Local Similarity 100.0%; Pred. No. 6.3e-114;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHVPAGSVASHLGTTSRSFYLTATLALCLVFTVATIMVLVQRTDSIPNSPDNVLPLG 60
Db 1 MHVPAGSVASHLGTTSRSFYLTATLALCLVFTVATIMVLVQRTDSIPNSPDNVLPLG 60
61 GNCSEDLICILKRAPFKSWAYLQVAKHLNKTLSWKNKDGILHGVRYQDGNLVIQFPGLY 120
Db 61 GNCSEDLICILKRAPFKSWAYLQVAKHLNKTLSWKNKDGILHGVRYQDGNLVIQFPGLY 120
QY 121 FIICQLQFLVQCPNNSVDLKLLELLINKHKKQALVTVCESGMOTKHVYQNLQSFLLDYQL 180
Db 121 FIICQLQFLVQCPNNSVDLKLLELLINKHKKQALVTVCESGMOTKHVYQNLQSFLLDYQL 180
QY 181 VNTTISVNVDTFQYIDTSTFPLENVLSIFLYSNSD 215
Db 181 VNTTISVNVDTFQYIDTSTFPLENVLSIFLYSNSD 215

RESULT 2
US-08-570-923-23
; Sequence 23, Application US/08570823
; Patent No. 5677430
; GENERAL INFORMATION:
; APPLICANT: Goodwin, Raymond G.
; APPLICANT: Smith, Craig A.
; APPLICANT: Armitage, Richard J.
; APPLICANT: Gruss, Hans-Jurgen
; TITLE OF INVENTION: No. 5677430el Cytokine That Binds CD30
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kathryn A. Seese, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple 7.1
; SOFTWARE: Microsoft Word, Version 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/570,923
; FILING DATE: 12-DEC-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/225,989
; FILING DATE: 12 APRIL 1994
; APPLICATION NUMBER: US 07/966,775
; FILING DATE: 27-OCT-1992
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 907,224
; FILING DATE: 01-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 899,660
; FILING DATE: 15-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 892,459
; FILING DATE: 02-JUN-1992

PRIOR APPLICATION DATA: US 889,717
; APPLICATION NUMBER: 26-MAY-1992
; FILING DATE: 26-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Seese, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2804-E
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 215 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-570-923-23

Query Match 100.0%; Score 1118; DB 1; Length 215;
Best Local Similarity 100.0%; Pred. No. 6.3e-114;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHVPAGSVASHLGTTSRSFYLTATLALCLVFTVATIMVLVQRTDSIPNSPDNVLPLG 60
Db 1 MHVPAGSVASHLGTTSRSFYLTATLALCLVFTVATIMVLVQRTDSIPNSPDNVLPLG 60
QY 61 GNCSEDLICILKRAPFKSWAYLQVAKHLNKTLSWKNKDGILHGVRYQDGNLVIQFPGLY 120
Db 61 GNCSEDLICILKRAPFKSWAYLQVAKHLNKTLSWKNKDGILHGVRYQDGNLVIQFPGLY 120
QY 121 FIICQLQFLVQCPNNSVDLKLLELLINKHKKQALVTVCESGMOTKHVYQNLQSFLLDYQL 180
Db 121 FIICQLQFLVQCPNNSVDLKLLELLINKHKKQALVTVCESGMOTKHVYQNLQSFLLDYQL 180
QY 181 VNTTISVNVDTFQYIDTSTFPLENVLSIFLYSNSD 215
Db 181 VNTTISVNVDTFQYIDTSTFPLENVLSIFLYSNSD 215

RESULT 3
US-08-580-014-230
; Sequence 23, Application US/08580014
; Patent No. 5753243
; GENERAL INFORMATION:
; APPLICANT: Goodwin, Raymond G.
; APPLICANT: Smith, Craig A.
; APPLICANT: Armitage, Richard J.
; APPLICANT: Gruss, Hans-Jurgen
; TITLE OF INVENTION: No. 5753203el Cytokine That Binds CD30
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kathryn A. Seese, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple 7.1
; SOFTWARE: Microsoft Word, Version 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/580,014
; FILING DATE: 20-DEC-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/225,989
; FILING DATE: 12 APRIL 1994
; APPLICATION NUMBER: US 07/966,775
; FILING DATE: 27-OCT-1992